

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/669,781A
Source: IFW16
Date Processed by STIC: 8/30/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

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- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

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Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>**> , **EFS Submission User Manual - ePAVE**)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06



IFW16

RAW SEQUENCE LISTING

DATE: 08/30/2006

PATENT APPLICATION: US/10/669,781A

TIME: 10:14:33

Input Set : F:\6031.79428 sequence.listing.ST25.txt

Output Set: N:\CRF4\08302006\J669781A.raw

3 <110> APPLICANT: Finnfeeds International, Ltd.
 5 <120> TITLE OF INVENTION: Phytase from Bacillus subtilis, gene encoding said phytase,
 6 method for its production and use
 8 <130> FILE REFERENCE: 79428
 10 <140> CURRENT APPLICATION NUMBER: 10/669,781A
 11 <141> CURRENT FILING DATE: 2003-09-24
 13 <160> NUMBER OF SEQ ID NOS: 36
 15 <170> SOFTWARE: PatentIn version 3.3

see pp 1-10

ERRORED SEQUENCES

E--> 17 <210> SEQ ID NO: ~~SEQ ID NO: 1~~

18 <211> LENGTH: 1290

19 <212> TYPE: DNA

20 <213> ORGANISM: Bacillus subtilis; Strain: B13

23 <220> FEATURE:

24 <221> NAME/KEY: CDS

25 <222> LOCATION: (91)..(1239)

27 <400> SEQUENCE: 1

28 cacatttgac aattttcaca aaaacttaac actgacaatc atgtatatat gttacaattg 60

30 aagtgcacgt tcataaaagg aggaagtaaa atg aat cat tca aaa aca ctt ttg 114

31 Met Asn His Ser Lys Thr Leu Leu

32 1 5

34 tta acc gcg gcg gcc gga ctg atg ctc aca tgc ggt gcg gtg tct tcc 162

35 Leu Thr Ala Ala Ala Gly Leu Met Leu Thr Cys Gly Ala Val Ser Ser

36 10 15 20

38 cag gca aag cat aag ctg tcc gat cct tat cat ttt acc gtg aat gca 210

39 Gln Ala Lys His Lys Leu Ser Asp Pro Tyr His Phe Thr Val Asn Ala

40 25 30 35 40

42 gcg gcg gaa acg gaa ccg gtt gat acg gcc ggt gac gcg gct gat gat 258

43 Ala Ala Glu Thr Glu Pro Val Asp Thr Ala Gly Asp Ala Ala Asp Asp

44 45 50 55

46 cct gcg att tgg ctg gac ccc aag act cct cag aac agc aaa ttg att 306

47 Pro Ala Ile Trp Leu Asp Pro Lys Thr Pro Gln Asn Ser Lys Leu Ile

48 60 65 70

50 acg acc aat aaa aaa tca ggt tta gtc gtt tac agc ctt gat ggt aag 354

51 Thr Thr Asn Lys Lys Ser Gly Leu Val Val Tyr Ser Leu Asp Gly Lys

52 75 80 85

54 atg ctt cat tcc tat aat acc ggg aag ctg aac aat gtc gat atc cgt 402

55 Met Leu His Ser Tyr Asn Thr Gly Lys Leu Asn Asn Val Asp Ile Arg

56 90 95 100

58 tat gat ttt ccg ttg aac ggc aaa aaa gtc gat atc gcg gca gca tcc 450

do not insert alphabetical headings. The CRF software will insert them for clarity.
 (global error)

Does Not Comply
 Corrected Diskette Needed

EX

RAW SEQUENCE LISTING

DATE: 08/30/2006

PATENT APPLICATION: US/10/669,781A

TIME: 10:14:33

Input Set : F:\6031.79428 sequence.listing.ST25.txt

Output Set: N:\CRF4\08302006\J669781A.raw

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59 Tyr Asp Phe Pro Leu Asn Gly Lys Lys Val Asp Ile Ala Ala Ala Ser
60 105 110 115 120
62 aat cgg tct gaa gga aaa aat acc att gag att tac gct att gat gga 498
63 Asn Arg Ser Glu Gly Lys Asn Thr Ile Glu Ile Tyr Ala Ile Asp Gly
64 125 130 135
66 aaa aac ggc aca tta caa agc atg aca gat cca gac cat ccg att gca 546
67 Lys Asn Gly Thr Leu Gln Ser Met Thr Asp Pro Asp His Pro Ile Ala
68 140 145 150
70 aca gca att aat gag gta tac ggt ttt acc tta tac cac agt caa aaa 594
71 Thr Ala Ile Asn Glu Val Tyr Gly Phe Thr Leu Tyr His Ser Gln Lys
72 155 160 165
74 aca gga aaa tat tac gcg atg gtg aca gga aaa gag ggt gaa ttt gaa 642
75 Thr Gly Lys Tyr Tyr Ala Met Val Thr Gly Lys Glu Gly Glu Phe Glu
76 170 175 180
78 caa tac gaa tta aag gcg gac aaa aat gga tac ata tcc ggc aaa aag 690
79 Gln Tyr Glu Leu Lys Ala Asp Lys Asn Gly Tyr Ile Ser Gly Lys Lys
80 185 190 195 200
82 gta cgg gcg ttt aaa atg aat tcc cag acg gaa ggg atg gca gca gac 738
83 Val Arg Ala Phe Lys Met Asn Ser Gln Thr Glu Gly Met Ala Ala Asp
84 205 210 215
86 gat gaa tac ggc agg ctt tat atc gca gaa gaa gat gag gcc att tgg 786
87 Asp Glu Tyr Gly Arg Leu Tyr Ile Ala Glu Glu Asp Glu Ala Ile Trp
88 220 225 230
90 aag ttc agc gcc gag ccg gac ggc ggc agt aac gga acg gtt atc gac 834
91 Lys Phe Ser Ala Glu Pro Asp Gly Gly Ser Asn Gly Thr Val Ile Asp
92 235 240 245
94 cgt gcc gac ggc agg cat tta act cgt gat att gaa gga ttg acg att 882
95 Arg Ala Asp Gly Arg His Leu Thr Arg Asp Ile Glu Gly Leu Thr Ile
96 250 255 260
98 tac tac gct gct gac ggg aaa ggc tat ctg atg gca tca agc cag gga 930
99 Tyr Tyr Ala Ala Asp Gly Lys Gly Tyr Leu Met Ala Ser Ser Gln Gly
100 265 270 275 280
102 aac agc agc tac gcc att tat gac aga caa gga aag aac aaa tat gtt 978
103 Asn Ser Ser Tyr Ala Ile Tyr Asp Arg Gln Gly Lys Asn Lys Tyr Val
104 285 290 295
106 gcg gat ttt cgc ata aca gac ggt cct gaa aca gac ggg aca agc gat 1026
107 Ala Asp Phe Arg Ile Thr Asp Gly Pro Glu Thr Asp Gly Thr Ser Asp
108 300 305 310
110 aca gac gga att gac gtt ctg ggt ttc gga ctg ggg cct gaa tat ccg 1074
111 Thr Asp Gly Ile Asp Val Leu Gly Phe Gly Leu Gly Pro Glu Tyr Pro
112 315 320 325
114 ttc ggt att ttt gtc gca cag gac ggt gaa aat ata gat cac ggc caa 1122
115 Phe Gly Ile Phe Val Ala Gln Asp Gly Glu Asn Ile Asp His Gly Gln
116 330 335 340
118 aag gcc aat caa aat ttt aaa atc gtg cca tgg gaa aga att gct gat 1170
119 Lys Ala Asn Gln Asn Phe Lys Ile Val Pro Trp Glu Arg Ile Ala Asp
120 345 350 355 360
122 caa atc ggt ttc cgc ccg ctg gca aat gaa cag gtt gac ccg aga aaa 1218
123 Gln Ile Gly Phe Arg Pro Leu Ala Asn Glu Gln Val Asp Pro Arg Lys

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RAW SEQUENCE LISTING

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Input Set : F:\6031.79428 sequence.listing.ST25.txt

Output Set: N:\CRF4\08302006\J669781A.raw

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124          365          370          375
126 ctg acc gac aga agc gga aaa taaacatgca aaaagcagct tatacaagct      1269
127 Leu Thr Asp Arg Ser Gly Lys
128          380
130 gcttttttgca tgtgaagaac g      1290
E--> 133 <210> SEQ ID NO: SEQ ID NO: 2
134 <211> LENGTH: 383
135 <212> TYPE: PRT
136 <213> ORGANISM: Bacillus subtilis; Strain: B13
OK-> 138 <400> SEQUENCE: 2
140 Met Asn His Ser Lys Thr Leu Leu Leu Thr Ala Ala Ala Gly Leu Met
141 1          5          10          15
144 Leu Thr Cys Gly Ala Val Ser Ser Gln Ala Lys His Lys Leu Ser Asp
145          20          25          30
148 Pro Tyr His Phe Thr Val Asn Ala Ala Ala Glu Thr Glu Pro Val Asp
149          35          40          45
152 Thr Ala Gly Asp Ala Ala Asp Asp Pro Ala Ile Trp Leu Asp Pro Lys
153          50          55          60
156 Thr Pro Gln Asn Ser Lys Leu Ile Thr Thr Asn Lys Lys Ser Gly Leu
157 65          70          75          80
160 Val Val Tyr Ser Leu Asp Gly Lys Met Leu His Ser Tyr Asn Thr Gly
161          85          90          95
164 Lys Leu Asn Asn Val Asp Ile Arg Tyr Asp Phe Pro Leu Asn Gly Lys
165          100         105         110
168 Lys Val Asp Ile Ala Ala Ala Ser Asn Arg Ser Glu Gly Lys Asn Thr
169          115         120         125
172 Ile Glu Ile Tyr Ala Ile Asp Gly Lys Asn Gly Thr Leu Gln Ser Met
173          130         135         140
176 Thr Asp Pro Asp His Pro Ile Ala Thr Ala Ile Asn Glu Val Tyr Gly
177 145         150         155         160
180 Phe Thr Leu Tyr His Ser Gln Lys Thr Gly Lys Tyr Tyr Ala Met Val
181          165         170         175
184 Thr Gly Lys Glu Gly Glu Phe Glu Gln Tyr Glu Leu Lys Ala Asp Lys
185          180         185         190
188 Asn Gly Tyr Ile Ser Gly Lys Lys Val Arg Ala Phe Lys Met Asn Ser
189          195         200         205
192 Gln Thr Glu Gly Met Ala Ala Asp Asp Glu Tyr Gly Arg Leu Tyr Ile
193          210         215         220
196 Ala Glu Glu Asp Glu Ala Ile Trp Lys Phe Ser Ala Glu Pro Asp Gly
197 225         230         235         240
200 Gly Ser Asn Gly Thr Val Ile Asp Arg Ala Asp Gly Arg His Leu Thr
201          245         250         255
204 Arg Asp Ile Glu Gly Leu Thr Ile Tyr Tyr Ala Ala Asp Gly Lys Gly
205          260         265         270
208 Tyr Leu Met Ala Ser Ser Gln Gly Asn Ser Ser Tyr Ala Ile Tyr Asp
209          275         280         285
212 Arg Gln Gly Lys Asn Lys Tyr Val Ala Asp Phe Arg Ile Thr Asp Gly
213          290         295         300
216 Pro Glu Thr Asp Gly Thr Ser Asp Thr Asp Gly Ile Asp Val Leu Gly

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Input Set : F:\6031.79428 sequence.listing.ST25.txt

Output Set: N:\CRF4\08302006\J669781A.raw

```

217 305          310          315          320
220 Phe Gly Leu Gly Pro Glu Tyr Pro Phe Gly Ile Phe Val Ala Gln Asp
221          325          330          335
224 Gly Glu Asn Ile Asp His Gly Gln Lys Ala Asn Gln Asn Phe Lys Ile
225          340          345          350
228 Val Pro Trp Glu Arg Ile Ala Asp Gln Ile Gly Phe Arg Pro Leu Ala
229          355          360          365
232 Asn Glu Gln Val Asp Pro Arg Lys Leu Thr Asp Arg Ser Gly Lys
233          370          375          380
E--> 236 <210> SEQ ID NO: SEQ ID NO:3
237 <211> LENGTH: 25
238 <212> TYPE: PRT
239 <213> ORGANISM: Bacillus subtilis
OK--> 241 <400> SEQUENCE: 3
243 Leu Ser Asp Pro Tyr His Phe Thr Val Asn Ala Ala Ala Glu Thr Glu
244 1          5          10          15
247 Pro Val Asp Thr Ala Gly Asp Ala Ala
248          20          25
E--> 251 <210> SEQ ID NO: SEQ ID NO:4
252 <211> LENGTH: 32
253 <212> TYPE: PRT
254 <213> ORGANISM: Bacillus subtilis
OK--> 256 <400> SEQUENCE: 4
258 Leu Ser Asp Pro Tyr His Phe Thr Val Asn Ala Ala Ala Glu Thr Glu
259 1          5          10          15
262 Pro Val Asp Thr Ala Gly Asp Ala Ala Asp Asp Pro Ala Ile Leu Asp
263          20          25          30
E--> 266 <210> SEQ ID NO: SEQ ID NO:5
267 <211> LENGTH: 8
268 <212> TYPE: PRT
269 <213> ORGANISM: Bacillus subtilis
OK--> 271 <400> SEQUENCE: 5
273 Tyr Tyr Ala Met Val Thr Gly Lys
274 1          5
E--> 277 <210> SEQ ID NO: SEQ ID NO:6
278 <211> LENGTH: 10
279 <212> TYPE: PRT
280 <213> ORGANISM: Bacillus subtilis
OK--> 282 <400> SEQUENCE: 6
284 Glu Gly Glu Phe Glu Gln Tyr Glu Leu Lys
285 1          5          10
E--> 288 <210> SEQ ID NO: SEQ ID NO:7
289 <211> LENGTH: 9
290 <212> TYPE: PRT
291 <213> ORGANISM: Bacillus subtilis
E--> 293 <400> SEQUENCE: 7
295 Met Leu His Ser Tyr Asn Thr Gly Lys
296 1          5
E--> 299 <210> SEQ ID NO: SEQ ID NO:8

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RAW SEQUENCE LISTING

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TIME: 10:14:34

Input Set : F:\6031.79428 sequence.listing.ST25.txt

Output Set: N:\CRF4\08302006\J669781A.raw

```

300 <211> LENGTH: 6
301 <212> TYPE: PRT
302 <213> ORGANISM: Bacillus subtilis
EX-> 304 <400> SEQUENCE: 8
306 Ile Val Pro Trp Glu Arg
307 1 5
E--> 310 <210> SEQ ID NO: SEQ ID NO:9
311 <211> LENGTH: 25
312 <212> TYPE: PRT
313 <213> ORGANISM: Bacillus subtilis
EX-> 315 <400> SEQUENCE: 9
317 Ile Val Pro Trp Glu Arg Ile Ala Asp Gln Ile Gly Phe Arg Pro Leu
318 1 5 10 15
321 Ala Asn Glu Gln Val Asp Pro Arg Lys
322 20 25
E--> 325 <210> SEQ ID NO: SEQ ID NO:10
326 <211> LENGTH: 30
327 <212> TYPE: PRT
328 <213> ORGANISM: Bacillus subtilis
EX-> 330 <400> SEQUENCE: 10
332 Asn Gly Thr Leu Gln Ser Met Thr Asp Pro Asp His Pro Ile Ala Thr
333 1 5 10 15
336 Ala Ile Asn Glu Val Tyr Gly Phe Thr Leu Trp His Ser Gln
337 20 25 30
E--> 340 <210> SEQ ID NO: SEQ ID NO:11
341 <211> LENGTH: 23
342 <212> TYPE: PRT
343 <213> ORGANISM: Bacillus subtilis
EX-> 345 <400> SEQUENCE: 11
347 Tyr Val Ala Asp Phe Arg Ile Thr Asp Gly Pro Glu Thr Asp Gly Thr
348 1 5 10 15
351 Ser Asp Asp Asp Gly Ile Ile
352 20
E--> 355 <210> SEQ ID NO: SEQ ID NO:12
356 <211> LENGTH: 7
357 <212> TYPE: PRT
358 <213> ORGANISM: Bacillus subtilis
EX-> 360 <400> SEQUENCE: 12
362 Leu Thr Asp Arg Ser Gly Lys
363 1 5
E--> 366 <210> SEQ ID NO: SEQ ID NO:13
367 <211> LENGTH: 13
368 <212> TYPE: PRT
369 <213> ORGANISM: Bacillus subtilis
EX-> 371 <400> SEQUENCE: 13
373 Val Asp Ile Ala Ala Ala Ser Asn Arg Ser Glu Gly Lys
374 1 5 10
E--> 377 <210> SEQ ID NO: SEQ ID NO:14
378 <211> LENGTH: 19

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RAW SEQUENCE LISTING

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TIME: 10:14:34

Input Set : F:\6031.79428 sequence.listing.ST25.txt

Output Set: N:\CRF4\08302006\J669781A.raw

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379 <212> TYPE: PRT
380 <213> ORGANISM: Bacillus subtilis
EX-> 382 <400> SEQUENCE: 14
384 Ile Ala Asp Gln Ile Gly Phe Arg Pro Leu Ala Asn Glu Gln Val Asp
385 1 5 10 15
388 Pro Arg Lys
E--> 392 <210> SEQ ID NO: SEQ ID NO:15
393 <211> LENGTH: 6
394 <212> TYPE: PRT
395 <213> ORGANISM: Bacillus subtilis
EX-> 397 <400> SEQUENCE: 15
399 Ala Asn Gln Asn Phe Lys
400 1 5
E--> 403 <210> SEQ ID NO: SEQ ID NO:16
404 <211> LENGTH: 5
405 <212> TYPE: PRT
406 <213> ORGANISM: Bacillus subtilis
EX-> 408 <400> SEQUENCE: 16
410 Val Arg Ala Phe Lys
411 1 5
E--> 414 <210> SEQ ID NO: SEQ ID NO:17
415 <211> LENGTH: 11
416 <212> TYPE: PRT
417 <213> ORGANISM: Bacillus subtilis
EX-> 419 <400> SEQUENCE: 17
421 Leu Asn Asn Val Asp Ile Arg Tyr Asp Phe Pro
422 1 5 10
E--> 425 <210> SEQ ID NO: SEQ ID NO:18
426 <211> LENGTH: 15
427 <212> TYPE: PRT
428 <213> ORGANISM: Bacillus subtilis
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432 Leu Asn Asn Val Asp Ile Arg Tyr Asp Phe Pro Leu Asn Gly Lys
433 1 5 10 15
E--> 436 <210> SEQ ID NO: SEQ ID NO:19
437 <211> LENGTH: 11
438 <212> TYPE: PRT
439 <213> ORGANISM: Bacillus subtilis
EX-> 441 <400> SEQUENCE: 19
443 Asn Thr Ile Glu Ile Tyr Ala Ile Asp Gly Lys
444 1 5 10
E--> 447 <210> SEQ ID NO: SEQ ID NO:20
448 <211> LENGTH: 11
449 <212> TYPE: PRT
450 <213> ORGANISM: Bacillus subtilis
EX-> 452 <400> SEQUENCE: 20
454 Ser Gly Leu Val Val Tyr Ser Leu Asp Gly Lys
455 1 5 10
E--> 458 <210> SEQ ID NO: SEQ ID NO:21

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RAW SEQUENCE LISTING

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TIME: 10:14:34

Input Set : F:\6031.79428 sequence.listing.ST25.txt

Output Set: N:\CRF4\08302006\J669781A.raw

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460 <212> TYPE: PRT
461 <213> ORGANISM: Bacillus subtilis
OK-> 463 <400> SEQUENCE: 21
465 Phe Ser Ala Glu Pro Asp Gly Gly Ser Asn Gly Thr Val Ile Asp Arg
466 1 5 10 15
469 Ala Asp Gly Arg His Leu
470 20
E--> 473 <210> SEQ ID NO: SEQ ID NO:22
474 <211> LENGTH: 23
475 <212> TYPE: DNA
476 <213> ORGANISM: Artificial
478 <220> FEATURE:
479 <223> OTHER INFORMATION: Synthesized
482 <220> FEATURE:
483 <221> NAME/KEY: modified_base
484 <222> LOCATION: (1)..(23)
OK-> 485 <223> OTHER INFORMATION: All Ns represents inosine
OK-> 487 <400> SEQUENCE: 22
W--> 488 tcngatccnt atcattttac ngT 23
E--> 491 <210> SEQ ID NO: SEQ ID NO:23
492 <211> LENGTH: 23
493 <212> TYPE: DNA
494 <213> ORGANISM: Artificial
496 <220> FEATURE:
497 <223> OTHER INFORMATION: Synthesized
500 <220> FEATURE:
501 <221> NAME/KEY: modified_base
502 <222> LOCATION: (1)..(23)
503 <223> OTHER INFORMATION: N represents inosine
OK-> 506 <400> SEQUENCE: 23
507 agmaggaaaat catancyrat atc 23
E--> 510 <210> SEQ ID NO: SEQ ID NO:24
511 <211> LENGTH: 22
512 <212> TYPE: DNA
513 <213> ORGANISM: Artificial
515 <220> FEATURE:
516 <223> OTHER INFORMATION: Synthesized
518 <220> FEATURE:
519 <221> NAME/KEY: modified_base
520 <222> LOCATION: (1)..(22)
521 <223> OTHER INFORMATION: All N's represent inosine
OK-> 523 <400> SEQUENCE: 24
524 cttcnganck rttnngangen gc 22
E--> 527 <210> SEQ ID NO: SEQ ID NO:25
528 <211> LENGTH: 20
529 <212> TYPE: DNA
530 <213> ORGANISM: Artificial
532 <220> FEATURE:

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Output Set: N:\CRF4\08302006\J669781A.raw

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533 <223> OTHER INFORMATION: Synthesized
536 <220> FEATURE:
537 <221> NAME/KEY: modified_base
538 <222> LOCATION: (1)..(20)
539 <223> OTHER INFORMATION: All N's represent inosine
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542 tgatcngcra tnckttccca 20
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546 <211> LENGTH: 20
547 <212> TYPE: DNA
548 <213> ORGANISM: Artificial
550 <220> FEATURE:
551 <223> OTHER INFORMATION: Synthesized
OK-> 553 <400> SEQUENCE: 26
554 gcratmggat gatcmggatc 20
E--> 557 <210> SEQ ID NO: SEQ ID NO+27
558 <211> LENGTH: 21
559 <212> TYPE: DNA
560 <213> ORGANISM: Artificial
562 <220> FEATURE:
563 <223> OTHER INFORMATION: Synthesized
566 <220> FEATURE:
567 <221> NAME/KEY: modified_base
568 <222> LOCATION: (1)..(21)
569 <223> OTHER INFORMATION: N represents inosine
OK-> 571 <400> SEQUENCE: 27
572 ttcataytgt tcaaattcnc c 21
E--> 575 <210> SEQ ID NO: SEQ ID NO+28
576 <211> LENGTH: 26
577 <212> TYPE: DNA
578 <213> ORGANISM: Artificial
580 <220> FEATURE:
581 <223> OTHER INFORMATION: Synthesized
584 <220> FEATURE:
585 <221> NAME/KEY: modified_base
586 <222> LOCATION: (1)..(26)
OK-> 587 <223> OTHER INFORMATION: All N's represent inosine
589 <400> SEQUENCE: 28
590 ttncngtrt tatangaatg narcat 26
E--> 593 <210> SEQ ID NO: SEQ ID NO+29
594 <211> LENGTH: 20
595 <212> TYPE: DNA
596 <213> ORGANISM: Artificial
598 <220> FEATURE:
599 <223> OTHER INFORMATION: Synthesized
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603 <221> NAME/KEY: modified_base
604 <222> LOCATION: (1)..(20)
605 <223> OTHER INFORMATION: N represents inosine

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TIME: 10:14:34

Input Set : F:\6031.79428 sequence.listing.ST25.txt

Output Set : N:\CRF4\08302006\J669781A.raw

OK-> 607 <400> SEQUENCE: 29
 608 ccacratng cataratttc 20
 E--> 611 <210> SEQ ID NO: ~~SEQ ID NO:30~~
 612 <211> LENGTH: 18
 613 <212> TYPE: DNA
 614 <213> ORGANISM: Artificial
 616 <220> FEATURE:
 617 <223> OTHER INFORMATION: Synthesized
 620 <220> FEATURE:
 621 <221> NAME/KEY: modified_base
 622 <222> LOCATION: (1)..(18)
 623 <223> OTHER INFORMATION: N represents inosine
 OK-> 626 <400> SEQUENCE: 30
 627 tttaaartty tgrttngc 18
 E--> 630 <210> SEQ ID NO: ~~SEQ ID NO:31~~
 631 <211> LENGTH: 18
 632 <212> TYPE: DNA
 633 <213> ORGANISM: Artificial
 635 <220> FEATURE:
 636 <223> OTHER INFORMATION: Synthesized
 639 <220> FEATURE:
 640 <221> NAME/KEY: modified_base
 641 <222> LOCATION: (1)..(18)
 642 <223> OTHER INFORMATION: All N's represent inosine
 OK-> 645 <400> SEQUENCE: 31
 646 tttncngtn accatngc 18
 E--> 649 <210> SEQ ID NO: ~~SEQ ID NO:32~~
 650 <211> LENGTH: 38
 651 <212> TYPE: DNA
 652 <213> ORGANISM: Artificial
 654 <220> FEATURE:
 655 <223> OTHER INFORMATION: Synthesized
 658 <220> FEATURE:
 659 <221> NAME/KEY: misc_feature
 660 <222> LOCATION: (21)..(21)
 661 <223> OTHER INFORMATION: n is a, c, g, or t
 OK-> 663 <400> SEQUENCE: 32
 664 gayccdtayc aytttyacdgt naaygcdgcd gcdgaaac 38
 E--> 667 <210> SEQ ID NO: ~~SEQ ID NO:33~~
 668 <211> LENGTH: 52
 669 <212> TYPE: DNA
 670 <213> ORGANISM: Artificial
 672 <220> FEATURE:
 673 <223> OTHER INFORMATION: Synthesized
 676 <220> FEATURE:
 677 <221> NAME/KEY: misc_feature
 678 <222> LOCATION: (7)..(14)
 679 <223> OTHER INFORMATION: Mfe I site
 681 <220> FEATURE:

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TIME: 10:14:34

Input Set : F:\6031.79428 sequence.listing.ST25.txt

Output Set: N:\CRF4\08302006\J669781A.raw

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682 <221> NAME/KEY: RBS
683 <222> LOCATION: (14)..(19)
685 <220> FEATURE:
686 <221> NAME/KEY: CDS
687 <222> LOCATION: (27)..(50)
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690 gtttctcaat tgaaggagga atttaa atg ctg tcc gat cct tat cat ttt ac      52
691                               Met Leu Ser Asp Pro Tyr His Phe
692                               1               5
E--> 695 <210> SEQ ID NO: SEQ ID NO:34
696 <211> LENGTH: 8
697 <212> TYPE: PRT
698 <213> ORGANISM: Artificial
700 <220> FEATURE:
OK-> 701 <223> OTHER INFORMATION: Synthetic Construct
OK-> 703 <400> SEQUENCE: 34
705 Met Leu Ser Asp Pro Tyr His Phe
706 1               5
E--> 709 <210> SEQ ID NO: SEQ ID NO:35
710 <211> LENGTH: 35
711 <212> TYPE: DNA
712 <213> ORGANISM: Artificial
714 <220> FEATURE:
715 <223> OTHER INFORMATION: Synthesized
718 <220> FEATURE:
719 <221> NAME/KEY: misc_feature
720 <222> LOCATION: (6)..(11)
721 <223> OTHER INFORMATION: Sal I site
OK-> 723 <400> SEQUENCE: 35
724 aataagtcga cgtacgaccg gattccggct gtgct      35
E--> 727 <210> SEQ ID NO: SEQ ID NO:36
728 <211> LENGTH: 34
729 <212> TYPE: DNA
730 <213> ORGANISM: Artificial
732 <220> FEATURE:
733 <223> OTHER INFORMATION: Synthesized
736 <220> FEATURE:
737 <221> NAME/KEY: misc_feature
738 <222> LOCATION: (6)..(11)
739 <223> OTHER INFORMATION: Bgl II site
OK-> 741 <400> SEQUENCE: 36
742 aataaagatc tttttccgct tctgtcggtc agtt      34

```

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/669,781A

DATE: 08/30/2006

TIME: 10:14:35

Input Set : F:\6031.79428 sequence.listing.ST25.txt

Output Set: N:\CRF4\08302006\J669781A.raw

L:17 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:27 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:1
 L:133 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:138 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:2
 L:236 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:241 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:3
 L:251 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:256 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:4
 L:266 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:271 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:5
 L:277 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:282 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:6
 L:288 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:293 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:7
 L:299 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:304 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:8
 L:310 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:315 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:9
 L:325 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:330 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:10
 L:340 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:345 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:11
 L:355 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:360 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:12
 L:366 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:371 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:13
 L:377 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:382 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:14
 L:392 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:397 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:15
 L:403 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:408 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:16
 L:414 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:419 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:17
 L:425 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:430 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:18
 L:436 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:441 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:19
 L:447 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:452 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:20
 L:458 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:463 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:21
 L:473 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:487 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:22
 L:488 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
 L:491 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:506 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:23
 M:341 Repeated in SeqNo=0

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VERIFICATION SUMMARY

DATE: 08/30/2006

PATENT APPLICATION: US/10/669,781A

TIME: 10:14:35

Input Set : F:\6031.79428 sequence.listing.ST25.txt

Output Set: N:\CRF4\08302006\J669781A.raw

L:510 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:523 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:24
L:527 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:541 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:25